

JUN 15 2005

STIC Biotechnology Systems Branch

**RAW SEQUENCE LISTING
ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/656,053A
Source: IFWO
Date Processed by STIC: 3/24/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



Raw Sequence Listing Error Summary

ERROR DETECTED**SUGGESTED CORRECTION****SERIAL NUMBER:**

10/656,053A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
36? and others
- 8 Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/656,053A

DATE: 03/24/2005
TIME: 14:45:41

Input Set : D:\ARAG003USD1.APP.txt
Output Set: N:\CRF4\03242005\J656053A.raw

3 <110> APPLICANT: GUEVERA, JR., JUAN G.
4 HOOGEVEEN, RON C.
5 MOORE, PAUL J.
7 <120> TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID VECTORS
9 <130> FILE REFERENCE: ARAG:003USD1
11 <140> CURRENT APPLICATION NUMBER: 10/656,053A
12 <141> CURRENT FILING DATE: 2003-09-05
14 <150> PRIOR APPLICATION NUMBER: 09/079,030
15 <151> PRIOR FILING DATE: 1998-05-14
17 <150> PRIOR APPLICATION NUMBER: 08/874,807
18 <151> PRIOR FILING DATE: 1997-06-13
20 <160> NUMBER OF SEQ ID NOS: 229
22 <170> SOFTWARE: PatentIn Ver. 2.1

do NOT use upper-case letter "O";
use numeral "0"
(zero)

*Does Not Comply
Corrected Diskette Needed*

pp1-5

see p. 4 for explanation

ERRORED SEQUENCES

1477 <210> SEQ ID NO: 36
1478 <212> TYPE: PRT
1479 <213> ORGANISM: Homo sapiens
E--> 1481 <211> LENGTH:
1481 <400> SEQUENCE: 36
E--> 1481 36
1610 <210> SEQ ID NO: 42
1611 <212> TYPE: PRT
1612 <213> ORGANISM: Homo sapiens
E--> 1614 <211> LENGTH:
1614 <400> SEQUENCE: 42
E--> 1614 42
2152 <210> SEQ ID NO: 64
2153 <212> TYPE: PRT
2154 <213> ORGANISM: Homo sapiens
E--> 2156 <211> LENGTH:
2156 <400> SEQUENCE: 64
E--> 2156 64
2160 <210> SEQ ID NO: 65
2161 <212> TYPE: PRT
2162 <213> ORGANISM: Homo sapiens
E--> 2164 <211> LENGTH:
2164 <400> SEQUENCE: 65
E--> 2164 65
2380 <210> SEQ ID NO: 81
2381 <212> TYPE: PRT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/656,053A

DATE: 03/24/2005
TIME: 14:45:41

Input Set : D:\ARAG003USD1.APP.txt
Output Set: N:\CRF4\03242005\J656053A.raw

2382 <213> ORGANISM: Homo sapiens
E--> 2384 <211> LENGTH:
2384 <400> SEQUENCE: 81
E--> 2384 81
2902 <210> SEQ ID NO: 104
2903 <212> TYPE: PRT
2904 <213> ORGANISM: Homo sapiens
E--> 2906 <211> LENGTH:
2906 <400> SEQUENCE: 104
E--> 2906 104
3079 <210> SEQ ID NO: 115
3080 <212> TYPE: PRT
3081 <213> ORGANISM: Homo sapiens
E--> 3083 <211> LENGTH:
3083 <400> SEQUENCE: 115
E--> 3083 115
3262 <210> SEQ ID NO: 120
3263 <212> TYPE: PRT
3264 <213> ORGANISM: Homo sapiens
E--> 3266 <211> LENGTH:
3266 <400> SEQUENCE: 120
E--> 3266 120
3396 <210> SEQ ID NO: 124
3397 <212> TYPE: PRT
3398 <213> ORGANISM: Homo sapiens
E--> 3400 <211> LENGTH:
3400 <400> SEQUENCE: 124
E--> 3400 124
3404 <210> SEQ ID NO: 125
3405 <212> TYPE: PRT
3406 <213> ORGANISM: Homo sapiens
E--> 3408 <211> LENGTH:
3408 <400> SEQUENCE: 125
E--> 3408 125
3967 <210> SEQ ID NO: 162
3968 <212> TYPE: PRT
3969 <213> ORGANISM: Homo sapiens
E--> 3971 <211> LENGTH:
3971 <400> SEQUENCE: 162
E--> 3971 162
4039 <210> SEQ ID NO: 167
4040 <212> TYPE: PRT
4041 <213> ORGANISM: Homo sapiens
E--> 4043 <211> LENGTH:
4043 <400> SEQUENCE: 167
E--> 4043 167
4481 <210> SEQ ID NO: 200
4482 <212> TYPE: PRT
4483 <213> ORGANISM: Homo sapiens

see p. 4

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/656,053A

DATE: 03/24/2005

TIME: 14:45:41

Input Set : D:\ARAG003USD1.APP.txt
Output Set: N:\CRF4\03242005\J656053A.raw

E--> 4485 <211> LENGTH:
4485 <400> SEQUENCE: 200
E--> 4485 200
4489 <210> SEQ ID NO: 201
4490 <212> TYPE: PRT
4491 <213> ORGANISM: Homo sapiens
E--> 4493 <211> LENGTH:
4493 <400> SEQUENCE: 201
E--> 4493 201
4556 <210> SEQ ID NO: 207
4557 <212> TYPE: PRT
4558 <213> ORGANISM: Homo sapiens
E--> 4560 <211> LENGTH:
4560 <400> SEQUENCE: 207
E--> 4560 207
4600 <210> SEQ ID NO: 211
4601 <212> TYPE: PRT
4602 <213> ORGANISM: Homo sapiens
E--> 4604 <211> LENGTH:
4604 <400> SEQUENCE: 211
E--> 4604 211
4668 <210> SEQ ID NO: 215
4669 <212> TYPE: PRT
4670 <213> ORGANISM: Homo sapiens
E--> 4672 <211> LENGTH:
4672 <400> SEQUENCE: 215
E--> 4672 215

see p.4

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4

<210> 36

<212> PRT

<213> Homo sapiens

<211> This mandatory residue identifier
and response are missing

<400> 36

no amino acids shown

if this sequence (and subsequent sequences)
are extentionally skipped, please use
the format shown in item 8 on
Error Summary Sheet



The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

10/656, 053A 5

<210> 2
<211> 3
<212> PRT
<213> Homo sapiens

<220>
<221> MOD_RES
<222> (2)
<223> x = anything

<400> 2
Pro Xaa Pro
1

please state "any amino acid" ("Xaa" can
only
represent a
single
amino
acid)

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.



VERIFICATION SUMMARY

PATENT APPLICATION: US/10/656,053A

DATE: 03/24/2005

TIME: 14:45:42

Input Set : D:\ARAG003USD1.APP.txt
Output Set: N:\CRF4\03242005\J656053A.raw

L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:1481 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:1481 M:301 E: (44) No Sequence Data was Shown, SEQ ID:36
L:1614 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:1614 M:301 E: (44) No Sequence Data was Shown, SEQ ID:42
L:2156 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:2156 M:301 E: (44) No Sequence Data was Shown, SEQ ID:64
L:2164 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:2164 M:301 E: (44) No Sequence Data was Shown, SEQ ID:65
L:2308 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0
L:2384 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:2384 M:301 E: (44) No Sequence Data was Shown, SEQ ID:81
L:2906 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:2906 M:301 E: (44) No Sequence Data was Shown, SEQ ID:104
L:3083 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:3083 M:301 E: (44) No Sequence Data was Shown, SEQ ID:115
L:3266 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:3266 M:301 E: (44) No Sequence Data was Shown, SEQ ID:120
L:3400 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:3400 M:301 E: (44) No Sequence Data was Shown, SEQ ID:124
L:3408 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:3408 M:301 E: (44) No Sequence Data was Shown, SEQ ID:125
L:3971 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:3971 M:301 E: (44) No Sequence Data was Shown, SEQ ID:162
L:4043 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4043 M:301 E: (44) No Sequence Data was Shown, SEQ ID:167
L:4485 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4485 M:301 E: (44) No Sequence Data was Shown, SEQ ID:200
L:4493 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4493 M:301 E: (44) No Sequence Data was Shown, SEQ ID:201
L:4560 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4560 M:301 E: (44) No Sequence Data was Shown, SEQ ID:207
L:4604 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4604 M:301 E: (44) No Sequence Data was Shown, SEQ ID:211
L:4672 M:282 E: Numeric Field Identifier Missing, <211> is required.
L:4672 M:301 E: (44) No Sequence Data was Shown, SEQ ID:215